

SEQUENCE LISTING

<110> Smith, Theresa H.
<120> PRO-INFLAMMATORY FIBRINOPEPTIDE
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<223> STRANDEDNESS: single
TOPOLOGY: both

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Ser Asp Trp Pro Phe Cys Ser Asp Glu Asp Trp Asn Tyr Lys Cys
35 40 45
Pro Ser Gly Cys Arg Met Lys Gly Leu Ile Asp Glu Val Asn Gln
50 55 60
Asp Phe Thr Asn Arg Ile Asn Lys Leu Lys Asn Ser Leu Phe Glu
65 70 75
Tyr Gln Lys Asn Asn Lys Asp Ser His Ser Leu Thr Thr Asn Ile
80 85 90
Met Glu Ile Leu Arg Gly Asp Phe Ser Ser Ala Asn Asn Arg Asp
95 100 105
Asn Thr Tyr Asn Arg Val Ser Glu Asp Leu Arg Ser Arg Ile Glu
110 115 120
Val Leu Lys Arg Lys Val Ile Glu Lys Val Gln His Ile Gln Leu
125 130 135
Leu Gln Lys Asn Val Arg Ala Gln Leu Val Asp Met Lys Arg Leu
140 145 150
Glu Val Asp Ile Asp Ile Lys Ile Arg Ser Cys Arg Gly Ser Cys
155 160 165
Ser Arg Ala Leu Ala Arg Glu Val Asp Leu Lys Asp Tyr Glu Asp
170 175 180
Gln Gln Lys Gln Leu Glu Gln Val Ile Ala Lys Asp Leu Leu Pro
185 190 195

Ser Arg Asp Arg Gln His Leu Pro Leu Ile Lys Met Lys Pro Val
200 205 210
Pro Asp Leu Val Pro Gly Asn Phe Lys Ser Gln Leu Gln Lys Val
215 220 225
Pro Pro Glu Trp Lys Ala Leu Thr Asp Met Pro Gln Met Arg Met
230 235 240
Glu Leu Glu Arg Pro Gly Gly Asn Glu Ile Thr Arg Gly Gly Ser
245 250 255
Thr Ser Tyr Gly Thr Gly Ser Glu Thr Glu Ser Pro Arg Asn Pro
260 265 270
Ser Ser Ala Gly Ser Trp Asn Ser Gly Ser Ser Gly Pro Gly Ser
275 280 285
Thr Gly Asn Arg Asn Pro Gly Ser Ser Gly Thr Gly Gly Thr Ala
290 295 300
Thr Trp Lys Pro Gly Ser Ser Gly Pro Gly Ser Thr Gly Ser Trp
305 310 315
Asn Ser Gly Ser Ser Gly Thr Gly Ser Thr Gly Asn Gln Asn Pro
320 325 330
Gly Ser Pro Arg Pro Gly Ser Thr Gly Thr Trp Asn Pro Gly Ser
335 340 345
Ser Glu Arg Gly Ser Ala Gly His Trp Thr Ser Glu Ser Ser Val
350 355 360
Ser Gly Ser Thr Gly Gln Trp His Ser Glu Ser Gly Ser Phe Arg
365 370 375
Pro Asp Ser Pro Gly Ser Gly Asn Ala Arg Pro Asn Asn Pro Asp
380 385 390
Trp Gly Thr Phe Glu Glu Val Ser Gly Asn Val Ser Pro Gly Thr
395 400 405
Arg Arg Glu Tyr His Thr Glu Lys Leu Val Thr Ser Lys Gly Asp
410 415 420
Lys Glu Leu Arg Thr Gly Lys Glu Lys Val Thr Ser Gly Ser Thr
425 430 435
Thr Thr Thr Arg Arg Ser Cys Ser Lys Thr Val Thr Lys Thr Val
440 445 450
Ile Gly Pro Asp Gly His Lys Glu Val Thr Lys Glu Val Val Thr
455 460 465
Ser Glu Asp Gly Ser Asp Cys Pro Glu Ala Met Asp Leu Gly Thr
470 475 480
Leu Ser Gly Ile Gly Thr Leu Asp Gly Phe Arg His Arg His Pro
485 490 495

Asp Glu Ala Ala Phe Phe Asp Thr Ala Ser Thr Gly Lys Thr Phe
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Pro Gly Phe Phe Ser Pro Met Leu Gly Glu Phe Val Ser Glu Thr
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Glu Ser Arg Gly Ser Glu Ser Gly Ile Phe Thr Asn Thr Lys Glu
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Ser Ser Ser His His Pro Gly Ile Ala Glu Phe Pro Ser Arg Gly
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Lys Ser Ser Ser Tyr Ser Lys Gln Phe Thr Ser Ser Thr Ser Tyr
560 565 570

Asn Arg Gly Asp Ser Thr Phe Glu Ser Lys Ser Tyr Lys Met Ala
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Asp Glu Ala Gly Ser Glu Ala Asp His Glu Gly Thr His Ser Thr
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Ser Pho Leu Gly Lys
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STRANDEDNESS: single
TOPOLOGY: linear
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Gly Pro Arg Pro